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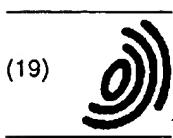
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Identities = 204/205 (99%), Positives = 204/205 (99%), Gaps = 1/205 (0%)
Frame = +3

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Sbjct: 138 MGAAFVASLRSNLSSATSRSEMNSSVGDLGVGGCSLWDDPARFIVVPAAYALALGLGLPA 120
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(54) Guanosine triphosphate-binding protein coupled receptors

(57) The object of the present invention is to provide a technique for efficiently extracting GPCR sequences from human genome sequences, thereby comprehensively identifying novel GPCRs. An original automatic

system for identifying GPCR sequences is disclosed, and 1035 novel GPCRs are successfully identified from the entire human genome by utilizing the system.